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OM protein - protein search, using sw model

Run on: December 29, 2005, 15:28:28 ; Search time 184 Seconds
 (without alignments)
 47.759 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTREGVLLKGKREEKPF 20

Scoring table: BLOSUM62

Gap open 10.0, Gap ext 0.5

Searched: 2443163 seqs, 419378781 residues

Total number of hits satisfying chosen parameters: 2443163

ARTICLES

static; vasotropic;
angiogenic;

卷之三

RESULT: 1
ADS13770 ID ADS13770 standard: peptide: 20 AA

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Result No.	Score	Query	Match	Length	DB	ID	Description
		Score	Match	Length	DB	ID	
1	106	100.0	20	8	ADSL3770		Adsl13770 Human Ang
2	106	100.0	20	8	ADSL13769		Adsl13769 Human Ang
3	106	100.0	26	8	ADSL13805		Adsl13805 Ang-1 lin
4	106	100.0	235	6	ABP32344		Aab32344 Human ang
5	106	100.0	261	8	ADL123636		Adl123636 Human Ang
6	106	100.0	298	8	ADL123638		Adl123638 Yeast GCN
7	106	100.0	310	8	ADL123640		Adl123640 Human CMP
8	106	100.0	312	8	ADL123642		Adl123642 Human COM
9	106	100.0	402	7	AAE38503		Aae38503 Human ang
10	106	100.0	402	9	AAE812448		Aae812448 Human ang
11	106	100.0	456	8	ADSL13776		Adsl13776 Mouse Ang
12	106	100.0	456	8	ADSL13775		Adsl13775 Human Ang
13	106	100.0	494	2	AAW47526		Aaw47526 Amino aci
14	106	100.0	498	2	AAW94603		Aaw94603 Human TIE
15	106	100.0	498	2	AAW101409		Aaw101409 Human TIE
16	106	100.0	498	2	AAW47530		Aaw47530 Amino aci
17	106	100.0	498	2	AAW47528		Aaw47528 Amino aci
18	106	100.0	498	3	AAV778905		Aav778905 Human ang
19	106	100.0	498	3	AAV778902		Aav778902 Human ang
20	106	100.0	498	3	AAE328391		Aae328391 Human ang
21	106	100.0	498	5	AAU177943		Aau177943 Amino aci
22	106	100.0	498	6	ABP58063		Abp58063 Human ang
23	106	100.0	498	6	AAE323447		Aae323447 Human ang
24	106	100.0	498	7	AAE338487		Aae338487 Mouse ang

related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, arterosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer, of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents an ECM-binding fragment of Ang-1 protein.

Sequence 20 AA:

Query Match Similarity 100.0%; Score 106; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-10; Mismatches 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 LCTPKGVLLKGKGRKEEKPF 20
Db 1 LCTPKGVLLKGKGRKEEKPF 20

RESULT 2
ID ADS13769 standard; peptide; 20 AA.
AC ADS13769;
XX DT-DEC-2004 (First entry)

DE Human Ang-1 protein ECM-binding fragment.

XX Ang-1; extracellular matrix; ECM; angiopoietin; cytostatic; vasotropic; antidiabetic; antiarthritic; cerebroprotective; antiangiogenic; gene therapy; human.
OS Homo sapiens.
PN WO2004076650-A2.

XX 10-BEP-2004.

XX 27-FEB-2004; 2004WO-US006101.

XX 27-FEB-2003; 2003US-0450582P.

(UYPB-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

DR N-PDB; ADS13787.

XX DR 2004-653413/63.

XX DR 2004-653413/63.

PT New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischaemia.
PT Claim 1; SEQ ID NO 1; 114pp; English.
XX The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of angiopoietin (Ang-1) protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving

CC ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patient with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, arterosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents an ECM-binding fragment of Ang-1 protein.

SQ Sequence 20 AA;

Query Match Similarity 100.0%; Score 106; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-10; Mismatches 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 LCTPKGVLLKGKGRKEEKPF 20
Db 1 LCTPKGVLLKGKGRKEEKPF 20

RESULT 3
ID ADS13805 standard; peptide; 26 AA.
AC ADS13805;
XX DT 02-DBC-2004 (first entry)
XX DE Ang-1 linker peptide region.
XX KW Ang-1; extracellular matrix; ECM; angiopoietin; cytostatic; vasotropic; antidiabetic; antiarthritic; cerebroprotective; antiangiogenic; gene therapy.
XX OS Homo sapiens.
XX PN WO2004076650-A2.
XX 10-BEP-2004.

XX 27-FEB-2004; 2004WO-US006101.

XX 27-FEB-2003; 2003US-0450582P.

(UYPB-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

DR New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischaemia.
PT The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-

CC binding fragment of angiopoietin (Ang-1) protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving

CC ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patient with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, arterosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents an ECM-binding fragment of Ang-1 protein.

SQ Sequence 20 AA;

Query Match Similarity 100.0%; Score 106; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e-10; Mismatches 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 LCTPKGVLLKGKGRKEEKPF 20
Db 1 LCTPKGVLLKGKGRKEEKPF 20

RESULT 4
ID ADS13805
AC ADS13805;
XX DT 02-DBC-2004 (first entry)
XX DE Ang-1 linker peptide region.
XX KW Ang-1; extracellular matrix; ECM; angiopoietin; cytostatic; vasotropic; antidiabetic; antiarthritic; cerebroprotective; antiangiogenic; gene therapy.
XX OS Homo sapiens.
XX PN WO2004076650-A2.
XX 10-BEP-2004.

XX 27-FEB-2004; 2004WO-US006101.
XX 27-FEB-2003; 2003US-0450582P.

(UYPB-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

PT New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischaemia.
PT The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-

CC binding fragment of angiopoietin (Ang-1) protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving

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binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, atherosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents a linker peptide region of Ang-1 protein.

Sequence 26 AA;

Query Match 100.0%; Score 106; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.e-03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREEEKPF 20
Db 7 LCTKEGVLLKGKREEEKPF 26

RESULT 4
AAB32344 standard; protein; 235 AA.
ID: AAB32344
AC: AAB32344;
DT: 24-MAR-2003 (first entry)

DE Human angiopoietin-1 (Ang-1) truncated protein #1.
XX Vascular endothelial growth factor; VEGF; angiogenesis; wound healing; bone growth; osteoporosis; osteoarthritis; bone reconstruction; ulcer; lesion; injury; trauma; periodontal condition; protein therapy; human; angiopoietin-1; Ang-1.
XX Homo sapiens.
XX WO200281851-A2.
XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011406.
XX 10-APR-2001; 2001US-00832355.
PA (GENV-) GENVEC INC.
PI Kovacs I, Kessler PD;
XX DR WPI; 2003-075536/07.

XX New fusion protein comprising a non-heparin-binding vascular endothelial growth factor (VEGF) peptide portion and a non-VEGF peptide portion and a non-VEGF peptide portion, which forms a biologically active multimer, and where the chimaeric molecule in its non-multimeric form is not biologically active. Also included are an isolated nucleic acid encoding the coiled coil chimaeric molecule, an expression vector

binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, atherosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents a linker peptide region of Ang-1 protein.

Sequence 235 AA;

Query Match 100.0%; Score 106; DB 6; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.e-08; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREEEKPF 20
Db 215 LCTKEGVLLKGKREEEKPF 234

RESULT 5
AD123636 standard; protein; 261 AA.
ID: AD123636
XX AD123636;
AC 22-APR-2004 (first entry)

DE Human Ang-1 fibrinogen-like domain/Propryoprysin signal.
XX Human; Ang-1; fibrinogen-like domain; Propryoprysin signal; KW angiopoietin; coiled-coil domain; cell growth; proliferation; matrix protein; transcription factor; growth factor; secretory protein; KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP; KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell; KW endothelial precursor cell.
XX Homo sapiens.
OS Synthetic.

XX US2003220476-A1.
XX 27-NOV-2003.
XX 18-OCT-2002; 2002US-00273180.
XX PR 21-MAY-2002; 2002US-0382541P.
XX PA (KOHG/) KOH G Y.
XX PI Koh GY;
XX WPI; 2004-010889/01.
DR N-PSDB; AD123635.

PT New coiled coil chimeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.
XX Disclosure; SEQ ID NO 2; 38pp; English.

CC The invention relates to a coiled coil chimaeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of a ligand or ligand binding domain of a receptor, which forms a biologically active multimer, and where the chimaeric molecule in its non-multimeric form is not biologically active. Also included are an isolated nucleic acid encoding the coiled coil chimaeric molecule, an expression vector

comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation, and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factors family, growth factor family or secretory protein family. The coiled coil domain is from cartilage matrix protein (COMP) or cartilage oligomeric matrix protein (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting a differential function and/or influencing the phenotype, such as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibrinogen-like domain of Ang-1 with a preprotrypsin leader.

Sequence 261 AA;

Query Match 100.0%; Score 106; DB 8; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.4e-08; Mismatches 0; Indels 0; Gaps 0;

Sequence 261 AA;

Query Match 100.0%; Score 106; DB 8; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.6e-08; Mismatches 0; Indels 0; Gaps 0;

Sequence 298 AA;

Query Match 100.0%; Score 106; DB 8; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.6e-08; Mismatches 0; Indels 0; Gaps 0;

Sequence 298 AA;

RESULT 6
ID AD123638

AD123638 standard; protein; 298 AA.

XX AD123638;

XX DT 22-APR-2004 (first entry)

XX XX Yeast Gcn4 coiled-coil domain/Human Ang-1 cDNA.

XX KW Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;

KW angiopoietin; coiled-coil domain; cell growth; proliferation;

KW matrix protein; transcription factor; growth factor; secretory protein;

KW cartilage matrix protein; COMP; cartilage oligomeric matrix protein; Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell; endothelial precursor cell; yeast.

XX OS Homo sapiens.

OS Saccharomyces cerevisiae.

OS Chimeric.

XX US2003220476-A1.

XX PD 27-NOV-2003.

XX PF 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

PI Koh GY;

XX DR WPI; 2004-010889/01.

DR N-PSDB; AD123637.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked

PT to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.

XX Example 5; SEQ ID NO 4; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a

CC coiled-coil domain linked to either a receptor binding domain of a ligand

CC or ligand binding domain of a receptor, which forms a biologically active

CC multimer, and where the chimaeric molecule in its non-multimeric form is
CC not biologically active. Also included are an isolated nucleic acid
CC encoding the coiled coil chimeric molecule, an expression vector, a soluble
CC comprising the nucleic acid, a host cell comprising the vector, a soluble
CC biologically active multimer comprising the coiled coil chimeric
CC molecule, promoting cell growth or proliferation, decreasing or
CC inhibiting ligand activity or cell proliferation and making a chimeric
CC molecule. The coiled coil chimeric molecule comprises a domain belonging
CC to a matrix protein family, transcription factor family, growth factor
CC family or secretory protein family. The coiled coil domain is from
CC a matrix protein family. The coiled coil domain is from
CC family or secretory protein family. The coiled coil domain is from
CC cartilage matrix protein (COMP) or cartilage oligomeric matrix protein
CC (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The
CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -
CC 2, -3 or -4. The chimeric molecules are useful for promoting or
CC inhibiting a differential function and/or influencing the phenotype, such
CC as growth, survival, contractility, migration and/or proliferation of
CC receptor-bearing cells such as endothelial cells, haematopoietic stem
CC cells and endothelial precursor cells. The present sequence represents
CC the fibrinogen-like domain of Ang-1 with a preprotrypsin leader. The present sequence represents
CC a coiled-coil domain of Ang-1 in a chimaeric protein with a coiled-

CC coil domain.

XX SQ Sequence 298 AA;

Query Match 100.0%; Score 106; DB 8; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.6e-08; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCPKEGVLLKGGRKREEKPF 20
Db 64 LCPKEGVLLKGGRKREEKPF 83

RESULT 7
ID AD123640
AD123640 standard; protein; 310 AA.

XX AC AD123640;

XX DT 22-APR-2004 (first entry)

XX DE Human CMP coiled-coil domain/Ang-1.

XX KW Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;

XX KW angiopoietin; coiled-coil domain; cell growth; proliferation;

XX KW matrix protein; transcription factor; growth factor; secretory protein;

XX KW cartilage matrix protein; COMP; cartilage oligomeric matrix protein; Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell; endothelial precursor cell.

XX KW Homo sapiens.

OS Synthetic.

XX US2003220476-A1.

XX PN 2002US-00273180.

XX PD 27-NOV-2003.

XX PF 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

PI Koh GY;

XX DR WPI; 2004-010889/01.

DR N-PSDB; AD123639.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked

PT to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.

XX Example 6; SEQ ID NO 6; 38pp; English.

The invention relates to a coiled coil chimaeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of a ligand or ligand binding domain of a receptor, which forms a biologically active multimer, and where the chimaeric molecule in its non-multimeric form is not biologically active. Also included are an isolated nucleic acid encoding the coiled coil chimaeric molecule, an expression vector comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimaeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor or secretory protein family. The coiled coil domain is from cartilage matrix protein (CMP) or cartilage oligomeric matrix protein (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The receptor-binding domain is a fibronogen-like domain of angiopoietin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting differential function and/or influencing the phenotype, such as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibronogen-like domain of Ang-1 in a chimaeric protein with a coiled-coil domain.

XX Sequence 310 AA;
 SQ Query Match 100.0%; Score 106; DB 8; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08; NMatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; NMatches 0; Indels 0; Gaps 0;
 Db 76 LCTREGVLLKGKREBKKF 95

RESULT 8
 ID ADI23642
 Human COMP coiled-coil domain/Ang-1.

XX AC ADI23642;
 XX DT 22-APR-2004 (First entry)
 XX DE Human COMP coiled-coil domain/Ang-1.
 XX KW Human; Ang-1; fibronogen-like domain; Preprotrypsin signal;
 KW angiopoietin1; coiled-coil domain; cell growth; proliferation;
 KW matrix protein; transcription factor; growth factor; secretory protein;
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;
 KW endothelial precursor cell.
 XX OS Homo sapiens.
 OS Synthetic.

XX PN US2003220476-A1.
 XX PD 27-NOV-2003.
 XX PP 18-OCT-2002; 2002US-00273180.
 XX PR 21-MAY-2002; 2002US-0382541P.
 XX PA (KORG/) KOH G Y.
 XX PI Koh GY;

XX DR WPI: 2004-010889/01.
 XX N-PSDB; ADI23641.
 XX PT New coiled coil chimeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.

XX PS Example 7; SEQ ID NO 8; 38pp; English.
 XX CC The invention relates to a coiled coil chimaeric molecule comprising a coiled-coil domain linked to either a receptor, which forms a biologically active or ligand binding domain of a receptor, which forms a biologically active multimer, and where the chimaeric molecule in its non-multimeric form is not biologically active. Also included are an isolated nucleic acid encoding the coiled coil chimaeric molecule, an expression vector comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimaeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor or secretory protein family. The coiled coil domain is from cartilage matrix protein (CMP) or cartilage oligomeric matrix protein (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The receptor-binding domain is a fibronogen-like domain of angiopoietin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting a differential function and/or influencing the phenotype, such as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibronogen-like domain of Ang-1 in a chimaeric protein with a coiled-coil domain.

XX SQ Sequence 312 AA;
 Query Match 100.0%; Score 106; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 20; Conservative 0; NMatches 0; Indels 0; Gaps 0;
 Db 78 LCTREGVLLKGKREBKKF 97

RESULT 9
 ID AAE38503 standard; protein; 402 AA.
 XX AC AAE38503;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human angiopoietin-1 #4.
 XX KW Angiopoietin-1; endothelium; cell proliferation; tumour; gene therapy;
 KW human.
 XX OS Homo sapiens.
 XX PN WO20030368165-A2.
 XX PD 21-AUG-2003.

XX PF 14-FEB-2003; 2003WO-US04595.
 XX PR 14-FEB-2002; 2002US-0356809P.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Ellis LM;
 XX DR WPI; 2003-697465/66.

XX PT Stabilizing the endothelium or reducing endothelial cell proliferation associated with a tumor comprises administering to a patient having a tumor angiopoietin-1 polypeptide.
 XX PS Disclosure; Page 139-140; 157pp; English.

Query Match 100.0%; Score 106; DB 8; Length 456;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREBEEKPF 20
 Db 222 LCTKEGVLLKGKREBEEKPF 241

RESULT 12
 ADSI3775 standard; protein; 456 AA.
 XX
 AC ADSI3775;
 XX
 DT 02-DEC-2004 (first entry)
 XX Human Ang-1 protein non-ECM-binding fragment.
 DE AAM47526;
 XX
 KW Ang-1; extracellular matrix; ECM; angiopoietin; cytostatic; vasotropic;
 KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 PN WO2004076650-A2.
 XX
 PD 10-SEP-2004.
 XX
 PP 27-FEB-2004; 2004W0-US006101.
 XX
 PR 27-FEB-2003; 2003US-0450582P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Yu Q;
 XX
 DR 2004-653413/53.
 DR N-PDBB; ADS13793.
 XX
 PR New pharmaceutical composition comprises a pharmaceutical carrier and an
 PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
 PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
 PT ischaemia.
 XX
 PS Claim 5; SEQ ID NO 7; 114pp; English.
 XX
 CC The invention relates to a pharmaceutical composition comprising a
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-
 CC binding fragment of angiopoietin (Ang-1) protein or a mutant Ang-1. Also
 CC provided are methods of treating an individual suspected of having
 CC coronary artery disease, vascular disease or a condition involving
 CC ischaemia; of promoting angiogenesis, endothelial survival and
 CC maintaining vascular integrity in an individual; of treating an
 CC individual suspected of having a disease related to lack of blood vessels
 CC to effectively promote angiogenesis in the patients with the disease
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
 CC arterosclerosis risk by maintaining the health and integrity of blood
 CC vessels; to assist the recovery of the patients who had stroke and the
 CC angioplasty procedure by promoting the growth/survival of endothelial
 CC cells and establish endothelial monolayer and inhibit excessive
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
 CC to treat patients with restenosis by inhibiting re-closure of blood
 CC vessel after inserting stents into blood vessels; to make stable and
 CC functional artificial blood vessels comprising using the composition
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
 CC of treating an individual suspected of having cancer; of preventing
 CC diabetes and/or arthritis. The pharmaceutical composition is
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
 CC angiogenesis, or arthritis. The present sequence represents a non-ECM-

CC binding fragment of Ang-1 protein.
 CC XX Sequence 456 AA;

Query Match 100.0%; Score 106; DB 8; Length 456;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREBEEKPF 20
 Db 222 LCTKEGVLLKGKREBEEKPF 241

RESULT 13
 AAM47526 standard; protein; 494 AA.
 XX
 AC AAM47526;
 XX
 DT 09-SEP-1998 (first entry)
 DE Amino acid sequence of chimeric TIE ligand 2N1C1F (chimera 4).
 XX
 KW Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation; tumour;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN WO9805779-A1.
 XX
 PD 12-FEB-1998.
 XX
 PP 01-AUG-1997; 97WO-US013557.
 XX
 PR 02-AUG-1996; 96US-0022999P.
 PR 25-OCT-1996;
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Davis S, Yancopoulos GD;
 XX
 DR WPI; 1998-145615/13.
 DR N-PDBB; AAV18613.
 XX
 PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
 PT healing.
 XX
 PS Claim 20; Fig 27; 2029P; English.

CC This is the amino acid sequence of the chimeric TIE ligand 2N1C1F, used
 CC in the method of the invention, involving the production of TIE-2 ligands
 CC which promote healing. The nucleic acids, vectors and host cells used in
 CC the method of the invention are useful for the recombinant production of
 CC the ligands. The ligands, etc. are useful for blocking blood vessel
 CC growth, promoting neovascularisation, promoting the growth or
 CC differentiation of a cell expressing the TIE receptor, blocking the
 CC growth or differentiation of a cell expressing the TIE receptor and for
 CC attenuating or preventing tumour growth in a human
 CC XX Sequence 494 AA;

Query Match 100.0%; Score 106; DB 2; Length 494;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREBEEKPF 20
 Db 260 LCTKEGVLLKGKREBEEKPF 279

RESULT 14
 AAR94603 standard; protein; 498 AA.
 ID AAR94603

RESULT 15

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OM protein - protein search, using SW model

Run on: December 29, 2005, 15:32:59 ; Search time 46 Seconds (without alignments)

35.946 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: LCTKEGVLLKGKREBBKPF 20

Scoring table: BL0SUM62

Gapext 0.5

Scoring table: Gapext 10.0 , Gapext 0.5

Scanned: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	106	100.0	478	2	US-08-740-223A-7		Sequence 7, Appli
2	106	100.0	478	2	US-09-709-188-7		Sequence 7, Appli
3	106	100.0	478	2	US-10-225-060-7		Sequence 7, Appli
4	106	100.0	495	2	US-08-740-223A-26		Sequence 26, Appli
5	106	100.0	495	2	US-09-709-188-26		Sequence 26, Appli
6	106	100.0	495	2	US-10-225-060-26		Sequence 26, Appli
7	106	100.0	497	2	US-08-740-223A-14		Sequence 14, Appli
8	106	100.0	497	2	US-09-709-188-14		Sequence 14, Appli
9	106	100.0	497	2	US-10-225-060-14		Sequence 14, Appli
10	106	100.0	498	1	US-08-373-579-2		Sequence 2, Appli
11	106	100.0	498	1	US-08-418-555-2		Sequence 2, Appli
12	106	100.0	498	1	US-08-665-926-2		Sequence 2, Appli
13	106	100.0	498	1	US-08-348-492-2		Sequence 2, Appli
14	106	100.0	498	2	US-09-162-337-2		Sequence 2, Appli
15	106	100.0	498	2	US-08-740-223A-2		Sequence 2, Appli
16	106	100.0	498	2	US-08-740-223A-20		Sequence 2, Appli
17	106	100.0	498	2	US-09-351-557-2		Sequence 2, Appli
18	106	100.0	498	2	US-09-561-100-2		Sequence 2, Appli
19	106	100.0	498	2	US-09-561-108-2		Sequence 2, Appli
20	106	100.0	498	2	US-09-351-543-2		Sequence 2, Appli
21	106	100.0	498	2	US-09-561-526-2		Sequence 5, Appli
22	106	100.0	498	2	US-09-202-491-5		Sequence 6, Appli
23	106	100.0	498	2	US-09-202-491-6		Sequence 2, Appli
24	106	100.0	498	2	US-08-817-318-2		Sequence 2, Appli
25	106	100.0	498	2	US-09-709-188-2		Sequence 20, Appli
26	106	100.0	498	2	US-09-099-188-20		Sequence 2, Appli
27	106	100.0	498	2	US-09-561-499-2		Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-740-223A-7

; Sequence 7, Application US/08740223A

; Patent No. 6265164

GENERAL INFORMATION:

; APPLICANT: David, et al.

; TITLE OF INVENTION: Expressed Ligand - Vascular

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Regeneron Pharmaceuticals, Inc.

; STREET: 777 Old Saw Mill Road

; CITY: Tarrytown

; STATE: NY

; COUNTRY: USA

; ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/740-223A

FILING DATE: 25-OCT-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/022/999

FILING DATE: 02-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Cober, Robert J.

REGISTRATION NUMBER: 36,108

REFERENCE/DOCKET NUMBER: REG 333

TELECOMMUNICATION INFORMATION:

TELEPHONE: 914-345-7400

TELEFAX: 914-345-7711

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 478 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Mature TLL protein

LOCATION: 1..478

OTHER INFORMATION:

US-08-740-223A-7

Query Match Best Local Similarity 100.0% ; Score 106; DB 2; Pred. No. 3.ee-09; Length 478;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Query 1 LCTKEGVLLKGKGRREBKKP 20
Db 244 LCTKEGVLLKGKGRREBKKP 263

RESULT 2
US-09-709-188-7
Sequence 7, Application US/09709188
Patent No. 6441137
GENERAL INFORMATION:
APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
FILE REFERENCE: REG 333-Z
CURRENT APPLICATION NUMBER: US/09/709,188
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 08/740,223
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-09-709-188-7

Query Match 100.0%; Score 106; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 LCTKEGVLLKGKGRREBKKP 20
Db 244 LCTKEGVLLKGKGRREBKKP 263

RESULT 3
US-10-225-060-7
Sequence 7, Application US/10225060
Patent No. 6625008
GENERAL INFORMATION:
APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
FILE REFERENCE: REG 333-Z
CURRENT APPLICATION NUMBER: US/10/225,060
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US/09/709,188
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 7
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-060-7

Query Match 100.0%; Score 106; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 LCTKEGVLLKGKGRREBKKP 20
Db 244 LCTKEGVLLKGKGRREBKKP 263

RESULT 4
US-08-740-223A-26
Sequence 26, Application US/08740223A
Patent No. 6255564
GENERAL INFORMATION:

APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Codeit, Robert J
REGISTRATION NUMBER: 36-108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7721
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: 2N1C1P (chimera 4)
LOCATION: 1..495
OTHER INFORMATION:
US-08-740-223A-26

Query Match 100.0%; Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 1 LCTKEGVLLKGKGRREBKKP 20
Db 261 LCTKEGVLLKGKGRREBKKP 280

RESULT 5
US-09-709-188-26
Sequence 26, Application US/09709188
Patent No. 6441137
GENERAL INFORMATION:
APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
FILE REFERENCE: REG 333-Z
CURRENT APPLICATION NUMBER: US/09/709,188
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 08/740,223
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 495
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chimeric

Sequence 2, Application US/08665926
 Patent No. 5851797
 GENERAL INFORMATION:
 APPLICANT: Valenzuela et al.
 TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
 TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill River Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10591-6707
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,926
 FILING DATE: 19-JUN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Robert J. Cobert
 REGISTRATION NUMBER: 36,108
 REFERENCE/DOCKET NUMBER: REG 330-H
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-2113
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-926-2

Query Match 100.0%; Score 106; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 3..3e-09; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 US-09-162-437-2
 Sequence 2, Application US/09162437
 Patent No. 6166185
 GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
 TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill River Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/162,437
 FILING DATE: 06-APR-1995
 CLASSIFICATION:
 PRIOR APPLICATION NUMBER: 08/418,595
 APPLICATION NUMBER: 08/418,595
 FILING DATE: 02-DEC-1994
 PRIOR APPLICATION NUMBER: US/08/373,579
 APPLICATION NUMBER: US/08/373,579
 FILING DATE: 17-JAN-1995
 PRIOR APPLICATION NUMBER: US/08/353,503
 APPLICATION NUMBER: US/08/353,503
 FILING DATE: 27-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/348,492
 FILING DATE: 02-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/330,261
 APPLICATION NUMBER: US/08/330,261
 FILING DATE: 27-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/319,932
 FILING DATE: 07-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Cobert, Robert J.

REGISTRATION NUMBER: 36.108
 REFERENCE/DOCKET NUMBER: REG 330-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-7721
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-162-431-2

Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRREEKPP 20
 Db 264 LCTKEGVLLKGKGRREEKPP 283

Search completed: December 29, 2005, 15:41:47
 Job time : 47 secs

RESULT 15
 US-08-740-223A-2
 Sequence 2, Application US/08740223A
 Patent No. 6265564
 GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 TITLE OF INVENTION: Intercellular Signalling Molecule
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill Road
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/740,223A
 FILING DATE: 25-OCT-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 60/022/999
 FILING DATE: 02-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Cobert, Robert J
 REGISTRATION NUMBER: 36,108
 REFERENCE/DOCKET NUMBER: REG 333
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 914-345-7400
 TELEFAX: 914-345-7721
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Human TIE-2 ligand 1
 LOCATION: 1..:498
 OTHER INFORMATION: from clone gt10 encoding hr1e-2
 OTHER INFORMATION: ligand 1

Query Match 100.0%; Score 106; DB 2; Length 498;

Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRREEKPP 20
 Db 264 LCTKEGVLLKGKGRREEKPP 283

RESULT 15
 US-08-740-223A-2
 Sequence 2, Application US/08740223A
 Patent No. 6265564
 GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 TITLE OF INVENTION: Intercellular Signalling Molecule
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill Road
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/740,223A
 FILING DATE: 25-OCT-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 60/022/999
 FILING DATE: 02-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Cobert, Robert J
 REGISTRATION NUMBER: 36,108
 REFERENCE/DOCKET NUMBER: REG 333
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 914-345-7400
 TELEFAX: 914-345-7721
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Human TIE-2 ligand 1
 LOCATION: 1..:498
 OTHER INFORMATION: from clone gt10 encoding hr1e-2
 OTHER INFORMATION: ligand 1

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1	106	100.0	20	4	US-10-789-222-1	Sequence 1, Appli	Sequence 1, Appli
2	2	106	100.0	20	4	US-10-789-222-1	Sequence 2, Appli	Sequence 2, Appli
3	3	106	100.0	235	3	US-09-832-355A-18	Sequence 18, Appli	Sequence 18, Appli
4	4	106	100.0	260	4	US-10-273-180-2	Sequence 2, Appli	Sequence 2, Appli
5	5	106	100.0	298	4	US-10-273-180-4	Sequence 4, Appli	Sequence 4, Appli
6	6	106	100.0	309	4	US-10-273-180-6	Sequence 6, Appli	Sequence 6, Appli
7	7	106	100.0	312	4	US-10-273-180-8	Sequence 8, Appli	Sequence 8, Appli
8	8	106	100.0	402	6	US-11-019-829-115	Sequence 36, Appli	Sequence 36, Appli
9	9	106	100.0	402	6	US-10-789-222-7	Sequence 7, Appli	Sequence 7, Appli
10	10	106	100.0	456	4	US-10-789-222-8	Sequence 115, Appli	Sequence 115, Appli
11	11	106	100.0	456	4	US-10-225-060-14	Sequence 26, Appli	Sequence 26, Appli
12	12	106	100.0	478	4	US-10-225-060-14	Sequence 26, Appli	Sequence 26, Appli
13	13	106	100.0	478	5	US-10-928-911-7	Sequence 14, Appli	Sequence 14, Appli
14	14	106	100.0	478	6	US-11-073-120-7	Sequence 14, Appli	Sequence 14, Appli
15	15	106	100.0	495	4	US-10-225-060-26	Sequence 2, Appli	Sequence 2, Appli
16	16	106	100.0	495	5	US-10-928-911-26	Sequence 13, Appli	Sequence 13, Appli
17	17	106	100.0	495	6	US-11-073-120-26	Sequence 15, Appli	Sequence 15, Appli
18	18	106	100.0	497	4	US-10-225-060-14	Sequence 14, Appli	Sequence 14, Appli
19	19	106	100.0	497	5	US-10-928-911-14	Sequence 14, Appli	Sequence 14, Appli
20	20	106	100.0	497	6	US-11-073-120-14	Sequence 14, Appli	Sequence 14, Appli
21	21	106	100.0	498	3	US-09-998-831-2	Sequence 13, Appli	Sequence 13, Appli
22	22	106	100.0	498	3	US-09-997-306-13	Sequence 2, Appli	Sequence 2, Appli
23	23	106	100.0	498	3	US-09-832-55A-15	Sequence 2, Appli	Sequence 2, Appli
24	24	106	100.0	498	3	US-09-998-833-2	Sequence 2, Appli	Sequence 2, Appli
25	25	106	100.0	498	4	US-10-179-744-2	Sequence 2, Appli	Sequence 2, Appli
26	26	106	100.0	498	4	US-10-186-177-2	Sequence 5, Appli	Sequence 5, Appli
27	27	106	100.0	498	4	US-10-215-224-5	US-10-789-222-14	US-10-789-222-14

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Query Match 100.0%; Score 106; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 18; LENGTH: 235; TYPE: PRT; ORGANISM: Homo sapiens
US-10-832-355A-18

Query Match 100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 4; LENGTH: 298; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-4

RESULT 3
US-09-832-355A-18
Sequence 18, Application US/09832355A
Publication No. US2003027751A1
GENERAL INFORMATION
APPLICANT: Kovacs, Imre
APPLICANT: Kessler, Paul
TITLE OF INVENTION: VEGF FUSION PROTEINS
FILE REFERENCE: 205654
CURRENT APPLICATION NUMBER: US/09/832,355A
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PatentIn version 3.0
SEQ_ID_NO 18
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-355A-18

Query Match 100.0%; Score 106; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.2e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 6; LENGTH: 309; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-6

Query Match 100.0%; Score 106; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 3e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 6; LENGTH: 309; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-6

RESULT 6
US-10-273-180-6
Sequence 6, Application US/10273180
Publication No. US20030220476A1
GENERAL INFORMATION
APPLICANT: KOH, Gou Young
TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
FILE REFERENCE: 10010-00001
CURRENT APPLICATION NUMBER: US/10/273,180
CURRENT FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ_ID_NO 6
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-273-180-6

Query Match 100.0%; Score 106; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 3e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 20; LENGTH: 309; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-6

RESULT 7
US-10-273-180-8
Sequence 8, Application US/10273180
Publication No. US20030220476A1
GENERAL INFORMATION
APPLICANT: KOH, Gou Young
TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
FILE REFERENCE: 10010-00001
CURRENT APPLICATION NUMBER: US/10/273,180
CURRENT FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ_ID_NO 8
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-10-273-180-8

Query Match 100.0%; Score 106; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 20; LENGTH: 312; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-8

RESULT 5
US-10-273-180-4
Sequence 4, Application US/10273180
Publication No. US20030220476A1
GENERAL INFORMATION
APPLICANT: KOH, Gou Young
TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
FILE REFERENCE: 10010-00001
SEQ_ID_NO 4
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapiens
US-10-273-180-4

Query Match 100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 20; LENGTH: 298; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-4

Query Match 100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 8; LENGTH: 298; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-8

Query Match 100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 20; LENGTH: 298; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-8

Query Match 100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NO: 78; LENGTH: 298; TYPE: PRT; ORGANISM: Homo sapiens
US-10-273-180-8

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RESULT 8
US-10-367-259A-36
; Sequence 36, Application US/10367259A
; GENERAL INFORMATION:
; APPLICANT: ELLIS, LEE M.
; TITLE OF INVENTION: ANGIOPOIETIN-1 IN THE TREATMENT OF DISEASE
; CURRENT APPLICATION NUMBER: US/10/367,259A
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,809
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-259A-36

Query Match 100.0%; Score 106; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mutants 0; Fragments 0;
TITLE OF INVENTION: Angiopoietin-1 in the treatment of disease
FILE REFERENCE: UTSC-698US
CURRENT APPLICATION NUMBER: US/10/367,259A
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/356,809
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
TYPE: PRT
ORGANISM: Homo sapiens
US-10-367-259A-36

RESULT 9
US-11-019-829-115
; Sequence 115, Application US/11019829
; Publication No. US20030136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; CURRENT APPLICATION NUMBER: US/11/019,829
; FILE REFERENCE: 22304
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: angiopoietin 1 variant 2
; LOCATION: (1) .. (402)
; OTHER INFORMATION: LocusID: 284; NM_139290
US-11-019-829-115

Query Match 100.0%; Score 106; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mutants 0; Fragments 0;
TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
FILE REFERENCE: 22304
CURRENT APPLICATION NUMBER: US/11/019,829
CURRENT FILING DATE: 2004-12-22
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 115
LENGTH: 402
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: angiopoietin 1 variant 2
LOCATION: (1) .. (402)
OTHER INFORMATION: LocusID: 284; NM_139290
US-11-019-829-115

Query Match 100.0%; Score 106; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mutants 0; Fragments 0;
TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
FILE REFERENCE: 22304
CURRENT APPLICATION NUMBER: US/11/019,829
CURRENT FILING DATE: 2004-12-22
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 115
LENGTH: 402
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: angiopoietin 1 variant 2
LOCATION: (1) .. (402)
OTHER INFORMATION: LocusID: 284; NM_139290
US-11-019-829-115

RESULT 10
US-10-789-222-7
; Sequence 7, Application US/10789222
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,582
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7

Query Match 100.0%; Score 106; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mutants 0; Fragments 0;
TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses
FILE REFERENCE: UPN0003-100 (P3115)
CURRENT APPLICATION NUMBER: US/10/789,222
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US 60/450,582
PRIOR FILING DATE: 2003-02-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 478;
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-060-7

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Qy 1 LCTKEGVLLKGKREBKEPF 20
 Db 244 LCTKEGVLLKGKREBKEPF 263

RESULT 13
 US-10-928-911-7 Sequence 7, Application US/10928911
 Publication No. US2005010609A1
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 Intercellular Signaling Molecule
 FILE REFERENCE: REG 333X
 CURRENT APPLICATION NUMBER: US/10/928, 911
 CURRENT FILING DATE: 2004-08-27
 PRIOR APPLICATION NUMBER: 10/245, 060
 PRIOR FILING DATE: 2002-08-21
 PRIOR APPLICATION NUMBER: 09/709, 188
 PRIOR FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: 08/740, 223
 PRIOR FILING DATE: 2000-11-09
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 478
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-928-911-7

Query Match 100.0%; Score 106; DB 5; Length 478;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREBKEPF 20
 Db 244 LCTKEGVLLKGKREBKEPF 263

RESULT 14
 US-11-073-120-7 Sequence 7, Application US/11073120
 Publication No. US2005018665A1
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 Intercellular Signaling Molecule
 FILE REFERENCE: REG 333X
 CURRENT APPLICATION NUMBER: US/11/073, 120
 CURRENT FILING DATE: 2005-03-04
 PRIOR APPLICATION NUMBER: 10/225, 060
 PRIOR FILING DATE: 2002-08-21
 PRIOR APPLICATION NUMBER: 09/709, 188
 PRIOR FILING DATE: 2000-11-09
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 478
 TYPE: PRT
 ORGANISM: Homo sapien
 US-11-073-120-7

Query Match 100.0%; Score 106; DB 6; Length 478;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKREBKEPF 20
 Db 244 LCTKEGVLLKGKREBKEPF 263

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	44	41.5	275	7	US-11-110-977-2		Sequence 2, Appli
2	43	40.6	415	7	US-11-182-946-6		Sequence 6, Appli
3	43	40.6	589	6	US-10-67-657-4826		Sequence 4826, Ap
4	42.5	40.1	163	6	US-10-793-626-5598		Sequence 2598, Ap
5	41	38.7	134	6	US-10-467-657-7860		Sequence 7860, Ap
6	41	38.7	394	6	US-10-467-657-7966		Sequence 7966, Ap
7	41	38.7	412	7	US-11-082-389-95		Sequence 96, Appli
8	40	37.7	257	6	US-10-632-150-40		Sequence 40, Appli
9	40	37.7	257	7	US-11-073-460-40		Sequence 40, Appli
10	40	37.7	257	7	US-11-071-057-047-3		Sequence 3, Appli
11	39	36.8	70	7	US-10-131-86A-280		Sequence 280, Appli
12	39	36.8	245	6	US-10-131-86A-280		Sequence 2, Appli
13	39	36.8	739	7	US-11-057-047-2		Sequence 6, Appli
14	39	36.8	761	7	US-11-057-047-6		Sequence 1, Appli
15	39	36.8	764	7	US-11-057-047-1		Sequence 1034, Ap
16	39	36.8	798	6	US-10-821-234-034		Sequence 842, Appli
17	38	35.8	213	6	US-10-995-561-842		Sequence 843, Appli
18	38	35.8	213	6	US-10-995-561-843		Sequence 845, Appli
19	38	35.8	213	6	US-10-995-561-845		Sequence 284, Appli
20	38	35.8	247	6	US-10-131-826A-284		Sequence 774, Appli
21	38	35.8	483	6	US-10-467-657-2774		Sequence 398, Appli
22	38	35.8	598	7	US-11-082-389-398		Sequence 6, Appli
23	38	35.8	739	7	US-11-107-028-6		Sequence 6506, Appli
24	38	35.8	968	7	US-11-004-43-1		Sequence 6506, Appli
25	37	34.9	145	6	US-10-467-657-5050		Sequence 6506, Appli

ALIGNMENTS

RESULT 1
US-11-110-977-2
; Sequence 2, Application US/11110977
; Publication No. US20050260682A1
; GENERAL INFORMATION:
; APPLICANT: Charmley, Patrick R.
; APPLICANT: Smith, Ryan C.
; APPLICANT: Argonza-Barrett, Rhodora H.
; APPLICANT: Fitzgibbon, Matthew P.
; APPLICANT: Wang, Kai P.
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psori
; FILE REFERENCE: CECII18764
; CURRENT APPLICATION NUMBER: US/11/110-977
; PRIORITY APPLICATION NUMBER: US/10/112,645
; PRIORITY FILING DATE: 2002-03-28
; PRIORITY APPLICATION NUMBER: US 60/280,514
; PRIORITY FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-110-977-2

Query Match Similarity 41.5%; Score 44; DB 7; Length 275;
Best Local Similarity 52.9%; Pred. No. 4.1;
Matches 9; Conservative 3; Mismatches 5; Indels 8; O; Gaps 0;
Qy 1 LCTKEGVLLKGKREEEF 17
Db 254 LGSSEVGLKNAEREQ 270

RESULT 2
US-11-182-946-6
; Sequence 6, Application US/11182946
; Publication No. US2005025510A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488-1280004
; CURRENT APPLICATION NUMBER: US/11/182-946
; CURRENT FILING DATE: 2005-07-18

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; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NO: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-182-945-6

Query Match 40.6%; Score 43; DB 7; Length 415;
Best Local Similarity 52.6%; Pred. No. 9.1;
Matches 10; Conservative 0; N mismatches 9;
Indels 0; Gaps 0;
RESULT 5
US-10-467-657-7860
; Sequence 7860, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabeta
; TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO: 7860
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-7860

Query Match 38.7%; Score 41; DB 6; Length 134;
Best Local Similarity 72.7%; Pred. No. 5.5;
Matches 8; Conservative 2; N mismatches 1;
Indels 0; Gaps 0;
RESULT 6
US-10-467-657-7966
; Sequence 7966, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabeta
; TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO: 7966
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-7966

Query Match 38.7%; Score 41; DB 6; Length 394;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 2; N mismatches 1;
Indels 0; Gaps 0;
RESULT 4
US-10-793-626-2598
; Sequence 2598, Application US/10793626
; Publication No. US2005255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMELLY, WILLIAM JOHN
; TITLE OF INVENTION: SPAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2598
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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Qy 6 GVLKKGKREB 16
 Db 276 GVLRLGTRKED 286

RESULT 7
 US-11-082-389-96
 ; Sequence 96, Application US/11082389
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zeider, Oskar
 ; APPLICANT: Haberhauser, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT
 ; FILE REFERENCE: BGI-131CPN
 ; CURRENT APPLICATION NUMBER: US/11/082,369
 ; CURRENT FILING DATE: 2005-03-16
 ; PRIOR APPLICATION NUMBER: US/09/603024
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US/60/141031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US/60/143262
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: US/60/151281
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19930487-4
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19930489-0
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931549-3
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931550-7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19932334-5
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19941379-7
 ; PRIOR FILING DATE: 1999-08-31
 ; Remaining Prior Application data removed - See File wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 446
 ; SEQ ID NO 96
 ; LENGTH: 412
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-11-082-389-96

Query Match 38.7%; Score 41; DB 7; length 412;
 Best Local Similarity 70.0%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEGVLLKGK 13
 Db 67 KDGVLKGE 76

RESULT 8
 US-10-632-150-40
 ; Sequence 40, Application US/10632150
 ; Publication No. US20050251871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chiaur, D.
 ; APPLICANT: Pagano, M.
 ; APPLICANT: Latres, E.
 ; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
 ; FILE REFERENCE: 5914-081
 ; CURRENT APPLICATION NUMBER: US/10/632,150
 ; CURRENT FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: US/09/385,219
 ; PRIOR FILING DATE: 1999-08-27

Query Match 37.7%; Score 40; DB 6; length 257;
 Best Local Similarity 46.7%; Pred. No. 17;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGKGRB 16
 Db 53 CQDGVLPEGGVEE 67

RESULT 9
 US-11-073-457-40
 ; Sequence 40, Application US/11073457
 ; Publication No. US2005020556A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, M.
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
 ; FILE REFERENCE: 5914-090-999
 ; CURRENT APPLICATION NUMBER: US/11/073,457
 ; CURRENT FILING DATE: 2005-03-04
 ; PRIOR APPLICATION NUMBER: 10/042,417
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 60/260,179
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 40
 ; LENGTH: 257
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-073-457-40

Query Match 37.7%; Score 40; DB 7; length 257;
 Best Local Similarity 46.7%; Pred. No. 17;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGKGRB 16
 Db 53 CQDGVLPEGGVEE 67

RESULT 10
 US-11-073-460-40
 ; Sequence 40, Application US/11073460
 ; Publication No. US20050272066A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, M.
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
 ; FILE REFERENCE: 5914-090-999
 ; CURRENT APPLICATION NUMBER: US/11/073,460
 ; CURRENT FILING DATE: 2005-03-04
 ; PRIOR APPLICATION NUMBER: 10/042,417
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 60/260,179
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 40

LENGTH: 257
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 US-11-073-46-40

Query Match 37.7%; Score 40; DB 7; Length 257;
 Best Local Similarity 46.7%; Pred. No. 17; Indels 0; Gaps 0;
 Matches 7; Conservative 4; Mismatches 4;

Qy 2 CTKEGVLLKGKREE 16
 :||: :|||
 Db 53 CQQBGLVPPGGVVEE 67

RESULT 11
 US-11-057-047-3
 Sequence 3, Application US/11057047
 Publication No. US20050260198A1
 GENERAL INFORMATION:
 / APPLICANT: Holers, Vernon
 / APPLICANT: Thurman, Joshua
 / APPLICANT: Taube, Christian
 / APPLICANT: Gelfand, Erwin
 / APPLICANT: Gilkeson, Gary
 / TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
 / TITLE OF INVENTION: Methods Related Thereto
 / FILE REFERENCE: 2843-66
 / CURRENT APPLICATION NUMBER: US/11/057,047
 / CURRENT FILING DATE: 2005-02-10
 / PRIOR APPLICATION NUMBER: 60/543,594
 / PRIOR FILING DATE: 2004-02-10
 / PRIOR APPLICATION NUMBER: 60/6316,239
 / PRIOR FILING DATE: 2004-12-14
 / PRIOR APPLICATION NUMBER: US04/015040
 / PRIOR FILING DATE: 2004-05-13
 / NUMBER OF SEQ ID NOS: 6
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO: 3
 / LENGTH: 70
 / TYPE: PRT
 / ORGANISM: *Homo sapiens*
 US-11-057-047-3

Query Match 36.8%; Score 39; DB 7; Length 70;
 Best Local Similarity 63.6%; Pred. No. 6.1; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 2;

Qy 2 CTKEGVLLKG 12
 :||: :|||
 Db 7 CSLEGVIKGG 17

RESULT 12
 US-10-131-826A-280
 / Sequence 280, Application US/10131826A
 / Publication No. US20050245730A1
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Beresini, Maureen
 / APPLICANT: DeForge, Laura
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Sherwood, Steven
 / APPLICANT: Smith, Victoria
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tomas, Daniel
 / APPLICANT: Watanabe, Colin K.
 / APPLICANT: Wood, William

Query Match 36.8%; Score 39; DB 7; Length 739;
 US-11-057-047-2

Best Local Similarity 63.6%; Pred. No. 73; Mismatches 2; Indels 0; Gaps 0; US-11-057-047-1

Query Match 36.8%; Score 39; DB 7; Length 764;

Best Local Similarity 63.6%; Pred. No. 76; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12

Db 12 CSLEGEVIEKG 22

RESULT 14

US-11-057-047-6

Sequence 6, Application US/11057047

Publication No. US20050260198A1

GENERAL INFORMATION:

APPLICANT: Holers, Vernon

APPLICANT: Thurman, Joshua

APPLICANT: Taube, Christian

APPLICANT: Gelfand, Erwin

APPLICANT: Gilkeson, Gary

TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and Methods Related Thereto

FILE REFERENCE: 2848-66

CURRENT APPLICATION NUMBER: US/11/057,047

PRIOR FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,594

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: 60/636,239

PRIOR FILING DATE: 2004-12-14

PRIOR APPLICATION NUMBER: US04/015040

PRIOR FILING DATE: 2004-05-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.3

SEQ ID NO 6

LENGTH: 761

TYPE: PRT

ORGANISM: Mus musculus

US-11-057-047-6

Query Match 36.8%; Score 39; DB 7; Length 761;

Best Local Similarity 63.6%; Pred. No. 76; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12

Db 34 CSLEGEVIEKG 44

RESULT 15

US-11-057-047-1

Sequence 1, Application US/11057047

Publication No. US20050260198A1

GENERAL INFORMATION:

APPLICANT: Holers, Vernon

APPLICANT: Thurman, Joshua

APPLICANT: Taube, Christian

APPLICANT: Gelfand, Erwin

APPLICANT: Gilkeson, Gary

TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and Methods Related Thereto

FILE REFERENCE: 2848-66

CURRENT APPLICATION NUMBER: US/11/057,047

PRIOR FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,594

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: 60/636,239

PRIOR FILING DATE: 2004-12-14

PRIOR APPLICATION NUMBER: US04/015040

PRIOR FILING DATE: 2004-05-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1

LENGTH: 764

TYPE: PRT

ORGANISM: Homo sapiens

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	30	43	40.6	1792	2
OM protein - protein search, using sw model		31	42.5	40.1	71	2
Run on:	December 29, 2005, 15:30:06 ; Search time 37 Seconds (without alignments)	32	42.5	40.1	204	2
Title:	US-10-789-222-1	33	42.5	40.1	284	2
Perfect score:	106	34	42	39.6	134	2
Sequence:	1 LCTKEGVLLKGKREEEKPF 20	35	42	39.6	137	2
Scoring table:	BLOSUM62	36	42	39.6	140	2
Gapop:	10.0 , Gapext 0.5	37	42	39.6	149	2
Searched:	283416 seqs, 96216763 residues	38	42	39.6	187	2
Total number of hits satisfying chosen parameters:	283416	39	42	39.6	188	1
Minimum DB seq length: 0		40	42	39.6	220	1
Maximum DB seq length: 2000000000		41	42	39.6	220	2
Post-processing: Minimum Match 0*		42	42	39.6	220	2
Maximum Match 100*		43	42	39.6	221	2
Database :	PIR 80.4	44	42	39.6	221	2
	1: pir1;*					
	2: pir2;*					
	3: pir3;*					
	4: pir4;*					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	46.2	658	2 B86599	metal transport P-metal transport P- cation-transportin probable metal tra- cation-transportin cation-transportin A5 antigen precurs
2	49	46.2	658	2 D72026	CRP synthase (EC 6 myoin heavy chain fibroblast growth probable integral
3	49	46.2	659	2 A81742	globulin-2 precurs hypothetical prote
4	49	46.2	659	2 B71479	hypothetical prote conserved hypothet
5	49	46.2	683	2 A81515	coat protein - Sou probable NADH2 deh
6	47	44.3	673	2 AG3521	hypothetical prote peptidylprolyl iso- ribose 5-phosphate
7	47	44.3	927	1 JQ0948	elongation factor translation elonga- 5-enolpyruvylshiki
8	46.5	43.9	591	1 SYHUTP	zinc finger protei legumain-like prote
9	46	43.4	389	2 S01371	nitrile/nitrite se nitrate/nitrite se
10	45	42.5	168	2 JG0184	
11	45	42.5	257	2 E71601	
12	45	42.5	450	2 S15675	
13	44	41.5	97	2 T29766	
14	44	41.5	141	2 T48751	
15	44	41.5	154	2 T20508	
16	44	41.5	228	2 C87184	
17	44	41.5	281	2 B81440	
18	44	41.5	396	2 A48336	
19	44	41.5	406	1 A70015	
20	44	41.5	486	2 S63384	
21	43	40.6	216	2 A56861	
22	43	40.6	227	2 F90249	
23	43	40.6	394	2 H97825	
24	43	40.6	394	2 C71672	
25	43	40.6	416	2 H69436	
26	43	40.6	477	2 T52382	
27	43	40.6	504	2 T10698	
28	43	40.6	590	2 C81911	
29	43	40.6	590	2 B81104	

ALIGNMENTS

RESULT 1						
B86599	metal transport P-type ATPase [Imported]	- Chlamydophila pneumoniae (strain J138)				
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae						
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004						
C;Accession: B86599						
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ito, R.						
Nucleic Acids Res. 28, 2311-2314, 2000						
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.						
A;Reference number: A86491; PMID:2030349; PMID:10871362						
A;Accession: B86599						
A;Status: preliminary						
A;Gene: zntA						
C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding domain homology <ATN>						
A;Molecule type: DNA						
A;Residues: 1-658 <STO>						
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:BA000008; NID:98979242; PMID:10871362						
A;Experimental source: strain J138						
C;Genetics:						

RESULT 2						
D72026	metal transport P-type ATPase - Chlamydophila pneumoniae (strain CML029)					
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae						
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004						
C;Accession: D72026						
R;Kalman, S.; Mitchell, W.; Marth, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999						
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.						
A;Reference number: A72000; PMID:99206606; PMID:10132388						
A;Accession: D72026						
A;Status: preliminary						
A;Gene: zntA						
A;Molecule type: DNA						
A;Residues: 1-658 <ARN>						
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620/Domain: ATPase nucleotide-binding domain homology <ATN>						
A;Experimental source: strain CML029						
C;Genetics:						

Query Match						
Qy	2	CTKEGLLKG 12				
Db	331	CAKGVLKG 341				
Matches	9	Conservative 0; Mismatches 0;				
Score	46.2%	DB 2; Length 658;				
DB	2	Prod. No. 16;				
Indels	2;					
Gaps	0;					
O						

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0; C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C; Accession: C81515
 A; Molecule type: DNA
 R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.;
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A; Reference number: A81500; MUID:20150255; PMID:10684935
 A; Accession: C81515
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-683 <REA>
 A; Cross-references: UNIPROT:Q9KIU0; UNIPARC:UPI000000CCC4; GB:AE002257; PMID:10684935
 A; Experimental source: strain AR39, HL cells
 C; Genetics:
 A; Gene: CP1001
 C; Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding domain homology <ATN>
 P; 503-615/Domain: ATPase nucleotide-binding domain homology <ATN>
 Query Match 46.2%; Score 49; DB 2; Length 683;
 Best Local Similarity 81.8%; Pred. No. 16;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CTKEGVLLKG 12
 Db 356 CAKHGVLLKG 366

RESULT 3
 A81742
 A; Status: preliminary
 C; Species: Chlamydia muridarum, Chlamydia muridarum (strain R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.;
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A; Reference number: A81500; MUID:20150255; PMID:10684935
 A; Molecule type: DNA
 A; Residues: 1-659 <TET>
 A; Cross-references: UNIPROT:Q9PLW9; UNIPARC:UPI00000577C9; GB:AE002277; PMID:10684935
 A; Experimental source: strain Nigg (MoPn)
 C; Genetics:
 A; Gene: TC0100
 C; Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding domain homology <ATN>
 P; 478-620/Domain: ATPase nucleotide-binding domain homology <ATN>
 Query Match 46.2%; Score 49; DB 2; Length 659;
 Best Local Similarity 81.8%; Pred. No. 16;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CTKEGVLLKG 12
 Db 331 CAKHGVLLKG 341

RESULT 4
 B71479
 A; Status: preliminary
 C; Species: Chlamydia trachomatis (serotype D, strain UW3/C)
 C; Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
 C; Accession: B71479
 R; Stephens, R.S.; Kalmann, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
 A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
 A; Reference number: A71570; MUID:39000809; PMID:9784136
 A; Accession: B71479
 A; Molecule type: DNA
 A; Residues: 1-659 <ARN>
 A; Cross-references: UNIPROT:Q84732; UNIPARC:UPI000003395; GB:AE001343; PMID:10684935
 A; Experimental source: serotype D, strain UW3/Cx
 C; Genetics:
 A; Gene: zntA
 C; Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding domain homology <ATN>
 P; 564-620/Domain: ATPase transduction domain homology <ATN>
 Query Match 46.2%; Score 49; DB 2; Length 659;
 Best Local Similarity 81.8%; Pred. No. 16;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 CTKEGVLLKG 12
 Db 331 CAKHGVLLKG 341

RESULT 5
 C81515
 C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (strain R; Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Fujisawa, H.; Neuron 7, 295-307, 1991
 A; Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology
 A; Reference number: JH0466; MUID:9133458; PMID:10684935
 A; Accession: JH0466
 A; Molecule type: mRNA
 A; Residues: 1-927 <TAK>
 A; Cross-references: UNIPARC:UPI0000171502; GB:DO10467; PMID:9222962; PMID:BA01077; NID:9222962; PMID:BA01077

A;Experimental source: tadpole, brain
 A;Note: this protein has motifs homologous to complement components C1r and C1s and to C
 C;Comment: This protein is a neuronal cell surface molecule involved in the neuronal rec
 C;Superfamily: Xenopus AS antigen; C1r/C1s repeat homology; discoidin I amino-terminal h
 C;Keywords: duplication; glycoprotein; transmembrane protein
 P;|-21;Domain: signal sequence #status predicted <SIC>
 P;42-927;Product: AS antigen #status predicted <ASA>
 P;42-138;Domain: C1r/C1s repeat homology <C1R1>
 P;447-262;Domain: C1r/C1s repeat homology <C1R2>
 P;474-474;Domain: discoidin I amino-terminal homology <DN1>
 P;430-584;Domain: discoidin I amino-terminal homology <DN2>
 P;446-812;Domain: MAM homology <AM>
 P;461-883;Domain: transmembrane #status predicted <TM>
 P;150,261,300,523,844;Binding site: carbohydrate (Asn) (covalent) #status predicted
 P;150,261,300,523,844;Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6 GVLKGKREBEEKPF 20 Score 44; DB 1; Length 927;
 Best Local Similarity 53.3%; Pred. No. 44; Indels 0; Gaps 0;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 RESULT 10
 JG0184 fibroblast growth factor - human
 C;Species: Homo sapiens (man)
 C;Accession: JG0184 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
 C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
 C;Title: Cloning and characterization of a cDNA encoding a novel fibroblast growth factor
 A;Reference number: JG0184
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-168 <KOK>
 A;Cross-references: UNIPARC:UP10000040663; GB:U76381
 C;Superfamily: Fibroblast growth factor

Query Match 6 GVLKGKREBEEKPF 20 Score 44; DB 1; Length 927;
 Best Local Similarity 53.3%; Pred. No. 44; Indels 0; Gaps 0;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 RESULT 11
 JG0184 fibroblast growth factor - human
 C;Species: Homo sapiens (man)
 C;Accession: JG0184 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
 C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
 C;Title: Cloning and characterization of a cDNA encoding a novel fibroblast growth factor
 A;Reference number: JG0184
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-168 <KOK>
 A;Cross-references: UNIPARC:UP10000040663; GB:U76381
 C;Superfamily: Fibroblast growth factor

Query Match 6 GVLKGKREBEEKPF 20 Score 44; DB 1; Length 927;
 Best Local Similarity 53.3%; Pred. No. 44; Indels 0; Gaps 0;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 RESULT 12
 E71601 probable integral membrane protein PFB0995w - malaria parasite (*Plasmodium falciparum*)
 C;Species: Plasmodium falciparum
 C;Accession: E71601 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
 C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
 Perteas, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
 Science 282, 1126-1132, 1998
 A;Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.
 A;Reference number: A71600; PMID:99021743; PMID:9804551
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Cross-references: 1-257 <GAR>
 A;Experimental source: clone 3D7
 C;Genetics:
 A;Gene: PFB0995w

Query Match 6 GVLKGKREBEEKPF 20 Score 44; DB 1; Length 927;
 Best Local Similarity 53.3%; Pred. No. 44; Indels 0; Gaps 0;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 RESULT 13
 S01371 myosin heavy chain, cardiac and skeletal muscle - eastern newt (fragment)
 C;Species: *Nocophthalmus viridescens*, *Triturus viridescens* (eastern newt)
 C;Accession: S01371; S57907 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C;Date: 30-Sep-1989 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 R;Casimir, C.M.; Gates, P.B.; Ross-Macdonald, P.B.; Jackson, J.P.; Patient, R.K.; Brocke
 J. Mol. Biol. 202, 287-296, 1988
 A;Title: Structure and expression of a new cardio-skeletal myosin gene. Implications for
 A;Reference number: S01371; PMID:9011957; PMID:2459393
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q7LZB4; UNIPARC:UPI00000177608
 A;Note: the sequence from fig. 7 is inconsistent with that from fig. 5 in having 64-1le,
 A;Accession: S67907

S15675 globulin-2 precursor - maize
C;Species: Zea mays (maize)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S15675
R;Wallace, N.H.; Krii, A.L.
Plant Physiol. 95, 973-975, 1991
A;Title: Nucleotide sequence of a cDNA clone corresponding to the maize globulin-2 gene.
A;Reference number: S15675
A;Accession: S15675
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-450 <WAL>
A;Cross-references: UNIPROT:Q7ML1Z8; UNIPARC:UPI0000177E41

Query Match 42.5%; Score 45; DB 2; Length 450;
Best Local Similarity 68.8%; Pred. No. 45;
Matches 11; Conservative 1; Mismatches 0; Indels 4; Gaps 1;
Qy . 4 KEG---VILKGGRKE 15
Db 95 KEGEGGVVILRGGRKE 110

RESULT 13
T29766 hypothetical protein ZC581.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29766
C;Accession: T29766
R;Natheron, B.; Gattung, S.; Le, T.T.
Submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid ZC581.
A;Reference number: Z20082
A;Accession: T29766
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-197 <WAT>
A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AP003134; PIDN:AAB54143.1; GSPDB:GN00019
A;Experimental source: strain Bristol N2; clone ZC581
C;Genetics:
A;Gene: CESP:ZC581.5
A;Map position: 1
A;Introns: 74/1

Query Match 41.5%; Score 44; DB 2; Length 97;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy . 5 EGVLJMGGRKEEE 17
Db 31 ERIMMKGGKNEBED 43

RESULT 14
T48751 hypothetical protein 8D4.250 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
C;Accession: T48751
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Hartmann, B.; Holland, R.; Nyakatura,
Submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24541
A;Accession: T48751
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <SCH>
A;Cross-references: UNIPARC:UPI0000179478; EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.250
A;Experimental source: cosmid contig 8D4, strain 74
C;Genetics:
A;Gene: NCSP:8D4.250
A;Map position: 2

S15675 globulin-2 precursor - maize
C;Species: Neurospora crassa hypothetical protein 8D4.250
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S15675
R;Wallace, N.H.; Krii, A.L.
Plant Physiol. 95, 973-975, 1991
A;Title: Nucleotide sequence of a cDNA clone corresponding to the maize globulin-2 gene.
A;Reference number: S15675
A;Accession: S15675
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-450 <WAL>
A;Cross-references: UNIPROT:Q7ML1Z8; UNIPARC:UPI0000177E41

Query Match 41.5%; Score 44; DB 2; Length 141;
Best Local Similarity 64.3%; Pred. No. 21;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy . 3 TKEGVLLKGGRKEE 16
Db 74 TKGKLSSGGKED 87

RESULT 15
T20508 hypothetical protein F02E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20508
R;Gray, I.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19285
A;Accession: T20508
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-154 <WIL>
A;Cross-references: UNIPROT:O013114; UNIPARC:UPI0000074F98; EMBL:Z81494; PIDN:CA04047.1;
A;Experimental source: clone F02E9
C;Genetics:
A;Gene: CESP:F02E9.1
A;Map position: 1
A;Introns: 29/2; 52/2; 80/3; 131/3

Query Match 41.5%; Score 44; DB 2; Length 154;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
Qy . 1 LCTKKG- -VILKGGRKEEK 18
Db 53 LDTKNGKFVLLQNSBNBEEK 72

Search completed: December 29, 2005, 15:40:56
Job time : 38 secs

Copyright (c) 1993 - 2005 Compugen Ltd.	Scoring table: BL050M22	Scoring table: BL050M22	Scoring table: BL050M22				
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run on: December 29, 2005, 15:29:18 ; Search time 230 Seconds (without alignments)	Post-processing: Maximum Match 0% Maximum Match 100% Listing first 45 summaries	UniProt 05.80:*	UniProt 05.80:*				
perfect score: 106	Sequence: 1 LCTKGVLJRKGSKREEEKPF 20	1: uniprot_sprot:*	1: uniprot_sprot:*				
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Minimum DB seq length: 0							
Maxximum DB seq length: 2000000000							
Post-processing: Maximum Match 0% Maximum Match 100% Listing first 45 summaries	Post-processing: Maximum Match 0% Maximum Match 100% Listing first 45 summaries	Post-processing: Maximum Match 0% Maximum Match 100% Listing first 45 summaries	Post-processing: Maximum Match 0% Maximum Match 100% Listing first 45 summaries				
Database : UniProt 05.80:*							
1: uniprot_sprot:*	1: uniprot_sprot:*	2: uniprot_trembl:*	2: uniprot_trembl:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES	SUMMARIES	SUMMARIES	SUMMARIES				
Result No.	Score	Query	Match	Length	DB	ID	Description
1	106	100.0	05YLW1_HUMAN	159	2	ANGP1_HUMAN	Q5Ylw1 homo sapien
2	106	100.0	ANGP1_HUMAN	498	1	ANGP1_MOUSE	Q15899 homo sapien
3	106	100.0	ANGP1_MOUSE	498	1	ANGP1_HUMAN	Q08538 mus musculus
4	106	100.0	Q5HYA0_HUMAN	498	2	Q6NNW7_MOUSE	Q5hyao homo sapien
5	106	100.0	Q6NNW7_MOUSE	498	2	Q8C2K6_MOUSE	Q6nnw7 mus musculus
6	106	100.0	Q8C2K6_MOUSE	498	2	Q9BDY8_PIG	Q8c2k6 mus musculus
7	96	90.6	Q9BDY8_PIG	498	2	Q9bdy8 sus scrofa	Q9bdy8 sus scrofa
8	89	5	Q8N6P1_HUMAN	147	2	Q8N6P3_homo_sapien	Q8n6p1 homo sapien
9	89	5	ANGP1_RAT	497	1	Q35460_rat	ANGP1_RAT
10	89	5	Q6A0F0_MOUSE	521	2	Q6a0f0 mus musculus	Q6a0f0 rat
11	86	5	Q60FCL_CANPA	497	2	Q60fcl canis familiaris	Q60fcl canis familiaris
12	85	5	ANGP1_BOVINA	481	1	Q6GNY4_XENLIA	ANGP1_BOVINA
13	76	71.7	Q6GNY4_XENLIA	504	2	Q6gn4 xenopus laevis	Q6gn4 xenopus laevis
14	59	55.7	Q9CUL6_MOUSE	383	2	Q9cul6 mus musculus	Q9cul6 mus musculus
15	54	51.9	Q4RNQ8_TETUNG	178	2	Q4rnq8 tetrardion n	Q4rnq8 tetrardion n
16	54	50.9	Q8H7M2_ORYSA	1040	2	Q8h7m2 oryza sativa	Q8h7m2 oryza sativa
17	53	50.0	Q8B486_9_FELAV	890	2	Q8b486_9_felav	Q8b486_9_felav
18	52	49.5	Q5XHAB_XENLIA	591	2	Q5xhab xenopus laevis	Q5xhab xenopus laevis
19	51	48.1	Q8I6J1_CIOSEA	181	2	Q8i6j1 clona savignyi	Q8i6j1 clona savignyi
20	51	48.1	Q9CST2_MOUSE	273	2	Q9cst2 mus musculus	Q9cst2 mus musculus
21	51	48.1	Q7Y188_ORYSA	566	2	Q7y188 oryza sativa	Q7y188 oryza sativa
22	51	48.1	Q7Y017_ORYSA	691	2	Q7y017 oryza sativa	Q7y017 oryza sativa
23	51	48.1	Q7DXD7_ORYSA	940	2	Q7xdx7 oryza sativa	Q7xdx7 oryza sativa
24	51	48.1	Q6L423_ORYSA	974	2	Q6l423 oryza sativa	Q6l423 oryza sativa
25	51	48.1	Q7XNN4_ORYSA	982	2	Q7xnn4 oryza sativa	Q7xnn4 oryza sativa
26	51	48.1	Q6E055_ORYSA	1059	2	Q6e055 oryza sativa	Q6e055 oryza sativa
27	51	48.1	Q5KQJ6_ORYSA	1109	2	Q5kqj6 oryza sativa	Q5kqj6 oryza sativa
28	51	48.1	Q75J31_ORYSA	1177	2	Q75j31 oryza sativa	Q75j31 oryza sativa
29	51	48.1	Q75HCL_ORYSA	1180	2	Q75hcl oryza sativa	Q75hcl oryza sativa
30	51	48.1	Q6L559_ORYSA	1198	2	Q6l559 oryza sativa	Q6l559 oryza sativa
31	51	48.1	Q4AGCT7_ORYSA	1198	2	Q4agct7 oryza sativa	Q4agct7 oryza sativa

RA	Yancopoulos G.D.;	FT	DOMAIN	284	498	Fibrinogen C-terminal.
RT	"Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by secretion-trap expression cloning.;"	FT	COILED	81	119	Potential.
RT	RL 871161-1169(1996).	FT	COILED	153	261	Potential.
[2]	NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.	FT	CARBOHYD	92	92	N-linked (GLCNAC. . .) (Potential).
RP	Nakatsukasa M., Konai K., Shiozawa S.;	FT	CARBOHYD	122	122	N-linked (GLCNAC. . .) (Potential).
RA	"Human angiopoietin-1 mRNA variant form.";	FT	CARBOHYD	154	154	N-linked (GLCNAC. . .) (Potential).
RT	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.	FT	CARBOHYD	243	243	N-linked (GLCNAC. . .) (Potential).
RL	NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.	FT	DISULFID	295	295	N-linked (GLCNAC. . .) (Potential).
[3]	RP	FT	DISULFID	286	315	By similarity.
RN	Shan Z.X., Yu X.Y., Lin Q.Y., Pu Y.H., Tan H.H., Zheng M., Lin S.G.;	FT	DISULFID	439	452	By similarity.
RA	"Human angiopoietin-1 mRNA variant forms.";	FT	VARIANT	269	269	Missing (in cell line T98G; may be due to exon skipping).
RT	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.	FT	VARIANT	269	269	/PTId=VAR_005940.
[4]	RN	SQ	SEQUENCE	498 AA:	57513 MW;	5D5FA63AEFB920 CRC64;
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].					
RC	TISSUE="Bone marrow";					
RX	MPIDLINE-96051387; PubMed=7584026;					
RA	Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.;					
RA	Sato S., Nagase T., Seki N., Ishikawa K.-I., Takata S.;					
RT	"Prediction of the Coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1.";					
RT	RNA Res. 1:27-35(1994).					
RN	[5]					
RP	SEQUENCE REVISION.					
RX	MEDLINE=2158533; PubMed=12168954;					
RA	Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;					
RT	"Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";					
RT	RT 9:99-106 (2002).					
CC	-1- FUNCTION: Binds and activates TIE2 receptor by inducing its tyrosine phosphorylation. Implicated in endothelial developmental processes later and distinct from that of VEGF. Appears to play a crucial role in mediating reciprocal interactions between the endothelium and surrounding matrix and mesenchyme. Mediates blood vessel maturation/stability. It may play an important role in the heart early development.					
CC	-1- SUBCELLULAR LOCATION: Secreted.					
CC	-1- PTM: Glycosylation.					
CC	-1- MISCELLANEOUS: It may have a potential therapeutic utility since it can be used for specifically targeting tumor vasculature or for promoting angiogenic processes in certain organs such as an ischemic heart.					
CC	-1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.					
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.					
CC	EMBL: U83508; AAB50557.1; - mRNA.					
CC	EMBL: AB04454; BAB91325.1; - mRNA.					
CC	EMBL: AY001745.1; - mRNA.					
CC	EMBL: AY124380; AAM52271.1; - mRNA.					
CC	EMBL: D13228; BAA02793.2; ALT_INIT; mRNA.					
CC	DR SP02671; 1P2D.					
CC	DR Ensembl: ENSG00000154188; Homo sapiens.					
CC	DR HGNC: HGNC:494; ANGPT1.					
CC	DR H-InvDB; HIX0007720; -.					
CC	DR MIM: 601667; -.					
CC	DR GO:0005102; F:receptor binding; TAS.					
CC	DR GO:0001165; P:signal transduction; TAS.					
CC	DR InterPro: IPR002181; Fibrinogen_C.					
CC	DR Pfam: PF00147; Fibrinogen_C; 1.					
CC	DR SMART: SM00186; FBG_1.					
CC	DR PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.					
CC	KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;					
CC	KW Glycoprotein; Polymorphism; Signal.					
CC	PT SIGNAL 1 15 Potential.					
CC	FT CHAIN 16 498 Angiopoietin-1.					
DR	EMBL: U83509; AAB50558.1; - mRNA.					
DR	HSSP: P02671; 1P2D.					
DR	DR Ensembl: ENSMUSG0000022309; Mus musculus.					
DR	MGI: MGI:108448; Angpt1.					
DR	GO: GO:0005615; C:extracellular space; TAS.					

GO: GO:0005172; F:vascular endothelial growth factor receptor. . . ; TAS.
 GO: GO:0007492; P:endothelial development; TAS.
 GO: GO:0007159; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
 InterPro: IP0002101; Fibrinogen_C.
 Pfam: PF00147; Fibrinogen_C_1.
 SMART: SM00136; FGG; 1.
 PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.
 KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
 KW Glycoprotein; Signal.

FT Potential. 19
 FT SIGNAL 1 19
 FT C-termina. 19
 FT CHAIN 20 498
 FT DOMAIN 284 498
 FT COILED 81 119
 FT COILED 153 261
 FT CARBOHYD 92 92
 FT CARBOHYD 122 122
 FT CARBOHYD 154 154
 FT CARBOHYD 243 243
 FT CARBOHYD 295 295
 FT DISULFID 286 315
 FT DISULFID 439 452
 SQ SEQUENCE 498 AA; 57505 MW; 285B4FB2C26D800 CRC64;
 Query Match Score 106; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1..8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRREEEKPP 20
 Db 264 LCTKEGVLLKGKGRREEEKPP 283

RESULT 4
 Q5HYAO HUMAN
 Q5HYAO_HUMAN PRELIMINARY; PRT; 498 AA.
 AC
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Hypothetical protein DKRZP68610222.
 GN Name=DKRZP68610222;
 OS Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;

RN NUCLEOTIDE SEQUENCE;
 TISSUE=Small intestine;
 The German cDNA Consortium;
 Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Obanger A., Pobo G.,
 RA Hahn M., Wiemann S.,
 RL Submitted (JAN-2005); to the EMBL/GenBank/DBJ databases.
 DR EMBL; B64884; CAA45984.1; -; mRNA.
 KW Hypothetical protein.

SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;

Query Match Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1..8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRREEEKPP 20
 Db 264 LCTKEGVLLKGKGRREEEKPP 283

RESULT 5
 Q6NWV7 MOUSE
 ID Q6NWV7_MOUSE PRELIMINARY; PRT; 498 AA.
 AC
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Angiopoietin 1.
 Name=Angpt1;
 Mus musculus (Mouse).
 OS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Shemesh C.M.,
 RA Hopkins R.P., Jordan R., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E.,
 RA Steapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Green E.D.,
 RA Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.X., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahay J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimeswood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schenrich A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RA Director MGC Project;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BCO067410; AAH67410.1; -; mRNA.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005172; P:vascular endothelial growth factor receptor. . . ; TAS.
 DR GO; GO:0007422; P:endothelial growth factor receptor. . . ; TAS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
 DR InterPro; IPR02181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG_C_DOMAIN; 1.
 SQ SEQUENCE 498 AA; 57513 MW; FC36F05A9E79074 CRC64;

Query Match Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1..8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGKGRREEEKPP 20
 Db 264 LCTKEGVLLKGKGRREEEKPP 283

RESULT 6
 Q8C2K6 MOUSE
 ID Q8C2K6_MOUSE PRELIMINARY;
 AC Q8C2K6;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-OCT-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus 2 days neonate thymus cells cDNA, RIKEN full-length enriched library, clone:B43 0016L03 product:angiopoietin, full insert sequence.
 DE Name=Angpt1;
 GN Mus musculus (Mouse).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

NUCLEOTIDE SEQUENCE.
 STRAIN=NO; TISSUE=Thymus;
 MEDLINE=9927253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 Carninci P., Hayashizaki Y.;
 "High-efficiency full-length cDNA cloning.;"
 Math. Enzymol. 303:19-44(1999).
 [2]
 RN
 NUCLEOTIDE SEQUENCE.
 RC
 STRAIN=NO; TISSUE=Thymus;
 MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500/
 Kawai J., Shinagawa A., Shitara K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Iwasa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 Saito T., Okazaki K., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H., Aishburner M., Baralov S., Casavant T.,
 Fleischmann W., Gasser T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quadebush J.,
 Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 Gustincich S., Hill D., Hoffmann M., Hune D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mazzarelli J., Mazzarelli P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shioota Y., Storch K.-F.,
 Suzuki H., Toyo-oka K., Wang K.H., Wetzig C., Whittaker C., Wilming L.,
 Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsbuki S.,
 Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection.;"
 Nature 409:685-690(2001).
 [3]
 RN
 NUCLEOTIDE SEQUENCE.
 RC
 STRAIN=NO; TISSUE=Thymus;
 The PANTOM Consortium,
 the RIKEN Genome Exploration Research Group Phase I & II Team;
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 Nature 420:563-573 (2002).
 [4]
 NUCLEOTIDE SEQUENCE.
 STRAIN=NO; TISSUE=Thymus;
 MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Konno H., Okazaki K., Muramatsu M., Hayashizaki Y.;
 "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RT
 Genome Res. 10:1617-1630 (2000).
 [5]
 NUCLEOTIDE SEQUENCE.
 STRAIN=NO; TISSUE=Thymus;
 MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA
 Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 Konno H., Akiyama J., Katsunai T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishida T., Harada A.,
 Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujikawa S., Inoue K., Inoue Y., Iwasa T., Ohara E., Watabiki M.,
 RA
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA
 Okazaki Y., Muramatsu M., Inoue Y., Kitra A., Hayashizaki Y.,
 RT
 "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL
 Genome Res. 10:1757-1771 (2000).
 [6]
 NUCLEOTIDE SEQUENCE.
 RC
 STRAIN=NO; TISSUE=Thymus;
 Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
 Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA
 Katoch H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S.,
 RA
 Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 Nishi K., Nomura K., Numazaki R., Ohno M., Ohzato N., Okazaki Y.,
 RA
 Saito R., Saitoh H., Sakai C., Sakai K., Sakazaki N., Sano H.,
 RA
 Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA
 Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
 Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR
 EMBL; AK088439; BAC40354.1; -; mRNA.
 DR
 HSSP; P02671; 1PZD.
 DR
 MGI; MGI:108448; Angpt1.
 DR
 InterPro; IPR02181; Fibrinogen_C.
 DR
 Pfam; PF00147; Fibrinogen_C.
 DR
 SMART; SM00186; FBG; 1.
 DR
 PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
 DR
 SEQUENCE; 498 AA; 5745 MW; 285D97468CSDB00 CRC64;
 Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. 0.1.8e-01;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy
 1 LCTKEGVLLKGGRREBKEKPF 20
 264 LCTKEGVLLKGGRREBKEKPF 283
 Do
 RESULT 7
 Q9BY8_PIG PIG PRELIMINARY; PRT; 498 AA.
 ID Q9BY8_PIG
 ID Q9BY8_PIG PRELIMINARY;
 AC Q9BY8_PIG
 AC Q9BY8_PIG PRELIMINARY;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DR 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Angiopoietin 1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Suina; Suidae;
 OC Sus scrofa (Pig).
 OC NCBi_TaxID=9823;
 OX [1]
 RN
 NUCLEOTIDE SEQUENCE.
 RP
 MEDLINE=21151163; PubMed=11230987; DOI=10.1016/S0008-6363(00)00295-9;
 RX
 RA
 Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
 RT
 "The angiopoietin-2 system in coronary artery endothelium prevents
 RT
 oxidized low-density lipoprotein-induced apoptosis.";
 RL
 Cardiovasc. Res. 49:872-881 (2001).
 DR
 EMBL; AF233227; AAC149921; -; mRNA.
 DR
 HSSP; P02671; 1PZD.
 DR
 InterPro; IPR02181; Fibrinogen_C.
 DR
 Pfam; PF00147; Fibrinogen_C.
 DR
 SMART; SM00186; FBG; 1.
 DR
 PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
 SQ
 SEQUENCE; 498 AA; 8C01C88F56061876 CRC64;
 Query Match 90.6%; Score 96; DB 2; Length 498;
 Best Local Similarity 90.0%; Pred. No. 6e-06;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy
 1 LCTKEGVLLKGGRREBKEKPF 20
 264 LCTKEGVLLKGGRREBKEKPF 283
 Do
 RESULT 8
 Q8NQP3_HUMAN PRELIMINARY; PRT; 147 AA.
 ID Q8NQP3_HUMAN PRELIMINARY;
 AC Q8NQP3
 AC Q8NQP3
 DR
 01-OCT-2002 (TREMBLrel. 22, Created)
 DT
 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT
 01-OCT-2003 (TREMBLrel. 23, Last annotation update)
 DE ANGPT1 protein.
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Hominoidea; Laurasiatheria; Euarchontoglires; Primates; Cetartiodactyla;
 OC NCBi_TaxID=9606;
 RN [1]

RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Prostate;	
RC	MEDLINE=2388857; PubMed=12477932; DOI=10.1073/pnas.242601899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klauser R.D., Collier P.S., Wagner L., Schenken C.M., Schuler G.D.,	
RA	Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahney J., Heitton B., Kerttman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Whitesley R.W., Touchman J.W., Green B.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U.,	
RA	Schnarch A., Schein J.-E., Jones S.J.M., Marra M.A.,	
RA	"Generation and initial analysis of more than 15,000 full-length human	
RA	and mouse cDNA sequences.";	
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]	
RC	TISSUE=Prostate;	
RA	Strausberg R.J.	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC029406; AAB29406.1; -; mRNA.	
DR	HSSP; P04671; 1FZD.	
DR	InterPro; IPR002181; Fibrinogen_C.	
DR	Pfam; PF00147; Fibrinogen_C; 1.	
DR	PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.	
DR	SMART; SM00186; Fibrinogen_C; 1.	
DR	SMART; SM00186; FBG; 1.	
DR	SEQUENCE 147 AA; 17314 MW; 68DD40DB06FA37E CRC64;	
SQ	Query Match Score 89.5; DB 2; Length 147;	
	Best Local Similarity 95.0%; Pred. No. 1.8e-05;	
	Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
Qy	1 LCTREGVLLKGKRKEEKKP 20	
Db	10 LCTKE-VLLKGKRKEEKKP 28	
RESULT 9	84.4%; Score 89.5; DB 1; Length 497;	
ID	ANGP1_RAT STANDARD; PRT; 497 AA.	
AC	Q35467; Q8K4Q4;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	10-MAY-2005 (Rel. 47, Last annotation update)	
DB	Angiopoietin-1 precursor (ANG-1).	
GN	Name=Angpt1;	
OS	Rattus norvegicus (Rat).	
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC	Muroidea; Muridae; Murinae; Rattus.	
NCBI_TaxID	10116;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=Nistar; TISSUE=Placenta;	
RC	MEDLINE=22346196; PubMed=12458684; DOI=10.1023/A:1020921818105;	
RA	Iizasa H., Bae S.H., Abashima T., Kitano T., Matsunaga N.,	
RA	Terasaki T., Kang Y.S., Nakashima E.,	
RT	"Augmented expression of the tight junction protein occludin in brain	
RT	endothelial cell line TR-BBB by rat angiopoietin-1 expressed in	
RT	baculovirus-infected sf plus insect cells.";	
RL	Pharm. Res. 19:1757-1760 (2002).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE OF	
RC	STRAIN=Sprague-Dawley; TISSUE=Placenta;	
RC	MEDLINE=8451164; PubMed=9776732;	
RC	Mandriota S.J., Pepper M.S.,	

RT	"Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia."	
RT	Circ. Res. 83:852-859 (1998).	
RL	-i- FUNCTION: Binds and activates TIE2 receptor by inducing its tyrosine phosphorylation. Implicated in endothelial development processes later and distinct from that of VEGF. Appears to play a crucial role in mediating reciprocal interactions between the endothelium and surrounding matrix and mesenchyme. Mediates blood vessel maturation/stability. It may play an important role in the heart early development.	
CC	-i- SUBCELLULAR LOCATION: Secreted.	
CC	-i- SIMILARITY: Contains 1 Fibrinogen C-terminal domain.	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	
CC	DR EMBL; AB080023; BAC10390.1; -; mRNA.	
DR	EMBL; AF030376; AAC78246.1; -; mRNA.	
DR	HSSP; P02671; 1FZD.	
DR	Ensembl; ENSRNOG0000005854; Rattus norvegicus.	
DR	RGD; 628896; Angpt1.	
DR	GO; GO:0001525; P: receptor binding; TAS.	
DR	DR InterPro; IPR002181; Fibrinogen C-terminal.	
DR	DR Pfam; PF00147; Fibrinogen_C; 1.	
DR	SMART; SM00166; FBG; 1.	
DR	PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.	
KW	Angiogenesis; Coiled coil; Developmental protein; Differentiation; Glycoprotein; Signal.	
KW	Potential.	
FT	FT SIGNAL 1 19	
FT	FT CHAIN 20 497	
FT	FT DOMAIN 283 497	
FT	FT COILED 81 119	
FT	FT COILED 153 261	
FT	FT CARBOHYD 92 92	
FT	FT CARBOHYD 122 122	
FT	FT CARBOHYD 154 154	
FT	FT CARBOHYD 243 243	
FT	FT CARBOHYD 294 294	
FT	FT DISULFID 285 314	
FT	FT DISULFID 438 451	
FT	FT CONFLICT 98 98	
FT	FT CONFLICT 172 172	
FT	FT CONFLICT 172 172	
FT	FT CONFLICT 189 189	
SEQUENCE	497 AA; 57461 MW; 08E66ABEF0D68AB CRC64;	
Query Match Best Local Similarity 95.0%; Pred. No. 6e-05;	Score 89.5; DB 1; Length 497;	
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	Best Local Similarity 95.0%; Pred. No. 6e-05;	
Qy	1 LCTREGVLLKGKRKEEKKP 20	
Db	10 LCTKE-VLLKGKRKEEKKP 28	
RESULT 10	84.4%; Score 89.5; DB 1; Length 497;	
ID	Q6A0FO_MOUSE PRELIMINARY;	
AC	Q6A0FO;	
DT	25-OCT-2004 (TREMBLrel.	
DT	25-OCT-2004 (TREMBLrel.	
DT	25-OCT-2004 (TREMBLrel.	
DE	MKIAP0003 protein (Fragment).	
GN	Name=Angpt1; Synonyms=MIKAP0003;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muridae; Murinae; Murinae; Mus.	
NCBI_TaxID	10090;	

AC	018940;	DT	16-OCT-2001 (Rel. 40, Created)
RP	NUCLEOTIDE SEQUENCE.	DT	16-OCT-2001 (Rel. 40, Last sequence update)
RC	TISSUE-Adult spleen;	DT	10-MAY-2005 (Rel. 40, Last annotation update)
RX	PubMed:1536895;	GN	Angiopoietin-1 precursor (ANG-1) (Fragment).
RA	Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,' Seino S., Nishimura M., Kaihoro T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H.,	GN	Name=ANGP1; Synonyms=ANG1;
RA	"Prediction of the coding sequences of mouse homologues of KIAA gene: IV. The complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";	OS	Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Laurasiatheria; Cetartiodactyla; Ruminantia; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
RA	DNA Res. 11:205-218 (2004).	NCBI_TAXID=9913;	NCBI_TAXID=9913;
RL	EMBL; AK12888; BAD32146.1; -; mRNA.	RN	[1]
DR	MGI; MGI:1084448; Angpt1.	RP	NUCLEOTIDE SEQUENCE.
DR	GO; GO:0005172; C:extracellular space; TAS.	RC	TISSUE=Ovary;
DR	GO; GO:0005172; P:vascular endothelial growth factor receptor. . . ; TAS.	RX	Medline=9054348; PubMed=9840613;
DR	GO; GO:0007492; P:endothelial development; TAS.	RA	Goede V., Schmidt T., Kimmela S., Kozian D., Augustin H.G., "Analysis of blood vessel maturation processes during cyclic ovarian angiogenesis.";
DR	GO; GO:00107169; P:transmembrane receptor protein tyrosine kinase. . . ; IDA.	RT	RT
DR	InterPro; IPR002181; Fibrinogen_C.	RL	RL
DR	Pfam; PF00147; Fibrinogen_C; 1.	RN	[2]
DR	SMART; SM00186; FBG; 1.	RP	NUCLEOTIDE SEQUENCE OF 91-200.
DR	PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.	RC	TISSUE=Liver;
FT	NON_TER 1. 1.	RX	Medline=98451564; PubMed=9776732;
SQ	SEQUENCE 521 AA: 60103 MW; 8E70617PA570DDFA CRC64;	RA	Mandriota S.J., Pepper M.S., "Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia.";
Qy	1 LCTKSEGVLKKGKREBKKP 20	RT	RT
Db	288 LCTKE-VLLKGKREBKKP 306	RL	Circ. Res. 83:852-859 (1998).
Qy	1 LCTKSEGVLKKGKREBKKP 20	CC	-!- FUNCTION: Binds and activates TIE2 receptor by inducing its tyrosine phosphorylation. Implicated in endothelial developmental processes later and distinct from that of VEGF. Appears to play a crucial role in mediating reciprocal interactions between the endothelium and surrounding matrix and mesenchyme. Mediates blood vessel maturation/ability. It may play an important role in the heart early development (By similarity).
Db	288 LCTKE-VLLKGKREBKKP 306	CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- DEVELOPMENTAL STAGE: Found to be expressed throughout the ovarian cycle.	CC	-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC	-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation of the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is removed.
CC	-!- PROSITE: PS00514; FIBRIN AG C DOMAIN; 1. Angiogenesis, Coiled coil; Developmental protein; Differentiation; Glycoprotein; Signal; 1. 15	CC	DR EMBL; AF093573; AAC61872.1; -; mRNA.
CC	-!- EMBL; AF032823; AAC78345.1; -; mRNA.	DR	DR HSSP; Q9UBWA; 1059.
CC	-!- InterPro; IPR002181; Fibrinogen_C; 1.	DR	DR InterPro; IPR002181; Fibrinogen_C; 1.
CC	-!- PFAM; PF00147; Fibrogen_C; 1.	DR	DR SMART; SM00186; FBG; 1.
CC	-!- PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. Angiogenesis, Coiled coil; Developmental protein; Differentiation; Glycoprotein; Signal; 1. 15	KW	KW
CC	-!- SIGNAL; 1. 15	FT	FT CARBOHYD 92 92
CC	-!- Angiopoietin-1.	FT	FT CHAIN 16 >481
CC	-!- Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT DOMAIN 283 >481
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT COILED 153 261
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT CARBOHYD 122 122
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT CARBOHYD 154 154
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT CARBOHYD 243 243
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT CARBOHYD 294 294
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT DISULFID 285 314
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT DISULFID 438 451
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT NON_TER 481 481
CC	-!- DR SMART; SM00186; FBG; 1.	SQ	SQ 5557 MW; 8EBC98D84FC2BB50 CRC64;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
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CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
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CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
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CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
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CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
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CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA; 481 AA;
CC	-!- RA Kato Y., Asano K., "Canis familiaris Angiopoietin-1 mRNA, complete cds.";	FT	FT 481 AA; 481 AA;
CC	-!- RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.	FT	FT 481 AA; 481 AA;
CC	-!- DR BMB1; AB192412; BAD5482.1; -; mRNA.	FT	FT 481 AA; 481 AA;
CC	-!- DR InterPro; IPR002181; Fibrinogen_C.	FT	FT 481 AA; 481 AA;
CC	-!- DR SMART; SM00186; FBG; 1.	FT	FT 481 AA; 481 AA;
CC	-!- DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1. SQ SEQUENCE 497 AA; 57415 MW; 06AFC2803E8P081 CRC64;	FT	FT 481 AA;

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Itoue Y., Kira A., Hayashizaki Y.;
 RT "Riken integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multipicillary sequencer. " ;
 Genome Res. 10:1757-1771(2000).
 [6]
 RN
 RP
 NUCLEOTIDE SEQUENCE.
 STPAIN=CS7BLJ6J; TISSUE="testis";
 RC
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F.,
 RA Imotani K., Ishii T., Itaya M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R., Ohno M.,
 RA Okazaki Y., Orido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibusawa K., Shiragawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toy T., Yamamura T., Yosumishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; ARX15496; BAB29870.2; -; mRNA.
 DR Ensembl; BNSMUSG0000024280; Mus musculus.
 MGI; MGI:11922184; Armc4.
 KW Hypothetical protein.
 PT TER 383 383
 SQ 383 AA; 43608 MN; AA688BAA4AACB01D CRC64;
 DR 55.7%; Score 59; DB 2; Length 383;
 DR 68.8%; Pred. No. 2.1;
 DR Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 DR 2 CTKEGVLLKGKREELP 17
 DR 262 CSTEGVFLNGKTEE 277

RESULT 15
 Q4RNUQ8 TETNG PRELIMINARY;
 ID Q4RNUQ8 "-"
 AC 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DE Chromosome 2 SCAF15010, whole genome shotgun sequence.
 GN ORFName=GSTENG00031451001;
 OS Tetradon nigroviridis (Green puffer).
 OC Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetradontoidae; Tetraodontidae; Tetradon.
 NCBI TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katsikas M., Vacherie B.,
 RA Biemont C., Skalli O., Cattolico L., Poulin J., De Barardini V.,
 RA Cruaud C., Duprat S., Brottier P., Courteau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKern K.J., McEwan P., Bossak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quétier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RT Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Genoscope; Whitehead Institute Centre for Genome Research;
 RA Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
 CC - I - CAUTION: The sequence shown here is derived from an

OTHER INFORMATION: 2N1C1F (chimera 4)

Query Match Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 LCTKEGVILKGGKREEEKPF 20
Db 261 LCTKEGVILKGGKREEEKPF 280

RESULT 6

US-10-225-060-26

; Sequence 26, Application US/1025060

; Patent No. 6825008

; GENERAL INFORMATION:

; APPLICANT: Davis et al.

; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling

; FILE REFERENCE: REG 333-2

; CURRENT APPLICATION NUMBER: US/10/225.060

; CURRENT FILING DATE: 2002-08-21

; PRIOR APPLICATION NUMBER: US/09/709,188

; PRIOR FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: 08/740,223

; PRIOR FILING DATE: 1996-10-25

; SEQ ID NO 26

; SOFTWARE: PatentIn version 3.1

; LENGTH: 495

; TYPE: PRT;

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Chimeric

; FEATURE:

; OTHER INFORMATION: 2N1C1F (chimera 4)

US-10-225-060-26

Query Match Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 LCTKEGVILKGGKREEEKPF 20
Db 261 LCTKEGVILKGGKREEEKPF 280

RESULT 7

US-08-740-223A-14

; Sequence 14, Application US/08740223A

; Patent No. 6265564

; GENERAL INFORMATION:

; APPLICANT: Davis, et al.

; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Regeneron Pharmaceuticals, Inc.

; STREET: 777 Old Saw Mill Road

; CITY: Tarrytown

; STATE: NY

; COUNTRY: USA

; ZIP: 10591

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; APPLICATION NUMBER: US/08/740,223A

; FILING DATE: 25-OCT-1996

; CLASSIFICATION: 536

PRIOR FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: 08/740,223
 PRIOR FILING DATE: 1996-10-25
 NUMBER OF SEQ ID NO: 30
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 14
 LENGTH: 497
 TYPE: PRT
 ORGANISM: Mus sp.
 US-10-225-060-14

Query Match 100.0%; Score 106; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEEKPF 20
 Db 264 LCTKEGVLLKGGRREEEKPF 283

RESULT 11
 US-08-418-595-2
 Sequence 2, Application US/08418595
 Patent No. 5814464
 GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill River Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/418,595
 FILING DATE: 06-APP-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/373,579
 FILING DATE: 17-JAN-1995
 APPLICATION NUMBER: US 08/353,503
 FILING DATE: 09-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,492
 FILING DATE: 02-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/330,261
 FILING DATE: 27-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/319,932
 FILING DATE: 07-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Cobert, Robert J.
 REGISTRATION NUMBER: 36,108
 REFERENCE/DOCKET NUMBER: REG 330-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-7721
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 498 amino acids
 TOPOLGY: linear
 MOLECULE TYPE: protein
 US-08-418-595-2

Query Match 100.0%; Score 106; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEEKPF 20
 Db 264 LCTKEGVLLKGGRREEEKPF 283

RESULT 12
 US-08-665-926-2